SCORE OVER LENGTH SEARCHES

Attached is a score over length search. This search was developed to overcome limitations in most standard search systems which favor large sequences with high scoring, but lesser overall identity over smaller sequences with higher overall identity. This search is especially useful for relatively small nucleic acid or polypeptide target sequences (antisense, fragments, probes, primers, RNAi, epitopes, haptens, etc.) claimed functionally via a form of hybridization and/or identity language and having defined upper and lower polynucleotide and or polypeptide length limits.

The score over length search is performed by first running the query sequence using examiner-specified identity and polynucleotide or protein length limit parameters, and saving 65,000 hits and 0 alignments from each desired database. The resulting output is reformatted using a Microsoft Word macro and is imported into Excel. The summary table data are then sorted by the ratio of score of each hit sequence divided by its length and the accession numbers for all hits below the examiner's desired score over length parameters are deleted. The remaining accession numbers are used to pull the corresponding sequences from the databases into subdatabases enriched for good hits and the query sequence is re-run against these subdatabases to yield the final results.

The score over length cutoff for this search is _100.7o_

Examiner Please Note: This cover sheet should be included when submitting results to be scanned.

151 749

From:	Chan, Christina
Sent:	Thursday, April 21, 2005 10:54 AM
To:	Steadman, David (AU1652); Schreiber, David
Subject:	RE: RUSH sequence search request for 09/855,750

Please rush. Thanks Chris

Chris Chan
TC 1600 New Hire Training Coordinator and SPE 1644
(571)-272-0841
Remsen, 3E89

-----Original Message-----
From:	Steadman, David (AU1652)
Sent:	Thursday, April 21, 2005 8:51 AM
To:	Chan, Christina
Subject:	RUSH sequence search request for 09/855,750

Ms. Chan,

I would like to request the RUSH sequence search listed below for an application that is +2 on my amended docket. If approved, please forward to D. Schreiber. Thank you very much.

David

NAME: David Steadman
AU: 1652
Date:04/21/05
Office: Remsen 2B05
Mailbox: Remsen 2C70

Please search the following sequence(s) in commercial and interference databases:

Score over length search of SEQ ID NO:1 with a minimum size of 15 and a maximum size of 2300. Please provide only 100% hits.

Please save results to diskette.

Thank you very much.

David J. Steadman, Ph.D.
Patent Examiner
Art Unit 1652 - Recombinant Enzymes
Office: Remsen 2B05
Mailbox: Remsen 2C70
(571) 272-0942

150041

From:	Steadman, David (AU1652)
Sent:	Thursday, March 31, 2005 7:21 AM
To:	Schreiber, David
Subject:	09/855,750 sequence search request

NAME: David Steadman
AU: 1652
Date:03/31/05
Office: Remsen 2B05
Mailbox: Remsen 2C70

Please search the following sequence(s) in commercial and interference databases:

1) Standard search of SEQ ID NO:2 against nucleic acid databases.

2) Standard search of nucleotides 247 to 2103 of SEQ ID NO:1 against nucleic acid databases.

3) Oligo search of SEQ ID NO:1 against nucleic acid databases.

Please save results to diskette.

Thank you very much.

David J. Steadman, Ph.D.
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(571) 272-0942